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1 CAGTGTGCTG GCGGCCGGC GCGAGCCGGC CGGGCCCGG TCGGGCCTCC
-26

GAAACC ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC
M V F L L S W V H W S
-26 -20

90 CTC GCC TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG
-15 L A L L L Y L H H A K W S Q
-10

GCT GCA CCC ATG GCA GAA GGA GGA GGG CAG AAT CAT CAC
A A P M A E G G G Q N H H
-1 +1 +5 +10

171 GAA GTG GTG AAG TTC ATG GAT GTC TAT CAG CGC AGC TAC TGC
13 E V V K F M D V Y Q R S Y C
+15 +20 +25

CAT CCA ATC GAG ACC CTG GTG GAC ATC TTC CAG GAG TAC
H P I E T L V D I F Q E Y
+30 +35

252 CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC TGT GTG CCC
40 P D E I E Y I F K P S C V P
+40 +45 +50

CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG
L M R C G G C C N D E G L
+55 +60 +65

333 GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT
67 E C V P T E E S N I T M Q I
+70 +75 +80

ATG CGG ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG
M R I K P H Q G Q H I G E
+85 +90

414 ATG AGC TTC CTA CAG CAC AAC AAA TGT GAA TGC AGA CCA AAG
94 M S F L Q H N K C E C R P K
+95 +100 +105

AAA GAT AGA CCA AGA CAA GAA AAT CCC TGT GGG CCT TGC
K D R A R Q E N P C G P C
+110 +115 +120

495 TCA GAG CGG AGA AAG CAT TTG TTT GTA CAA GAT CCG CAG ACG
121 S E R R K H L F V Q D P Q T
+125 +130

TGT AAA TGT TCC TGC AAA AAC ACA GAC TCG CGT TGC AAG
C K C S C K N T D S R C K
+135 +140 +145



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576 GCG AGG CAG CTT GAG TTA AAC GAA CGT ACT TGC AGA TGT GAC
148 A R Q L E L N E R T C R C D
+150 +155 +160

AAG CCG AGG CGG TGA GCCGGGCA GGAGGAAGGA GCCTCCCTCA
K P R R O
+165

661 GGGTTTCGGG AACCAGATCT CTCACCAGGA AAGACTGATA CAGAACGATC
GATACAGAAA CCACGCTGCC GCCACCACAC CATCACCATC GACAGAACAG

761 TCCTTAATCC AGAACCTGA AATGAAGGAA GAGGAGACTC TGCAGAGC
ACTTTGGGTC CGGAGGGCGA GACTCCGGCG GAAGCATTCC CGGGCGGGTG

861 ACCCAGCACG GTCCCTCTTG GAATTGGATT CGCCATTAA TTTTCTTGC
TGCTAAATCA CCGAGCCCGG AAGATTAGAG AGTTTTATTT CTGGGATTCC

961 TGTAGACACA CCGCGGCCGC CAGCACACTG

FIG._1B

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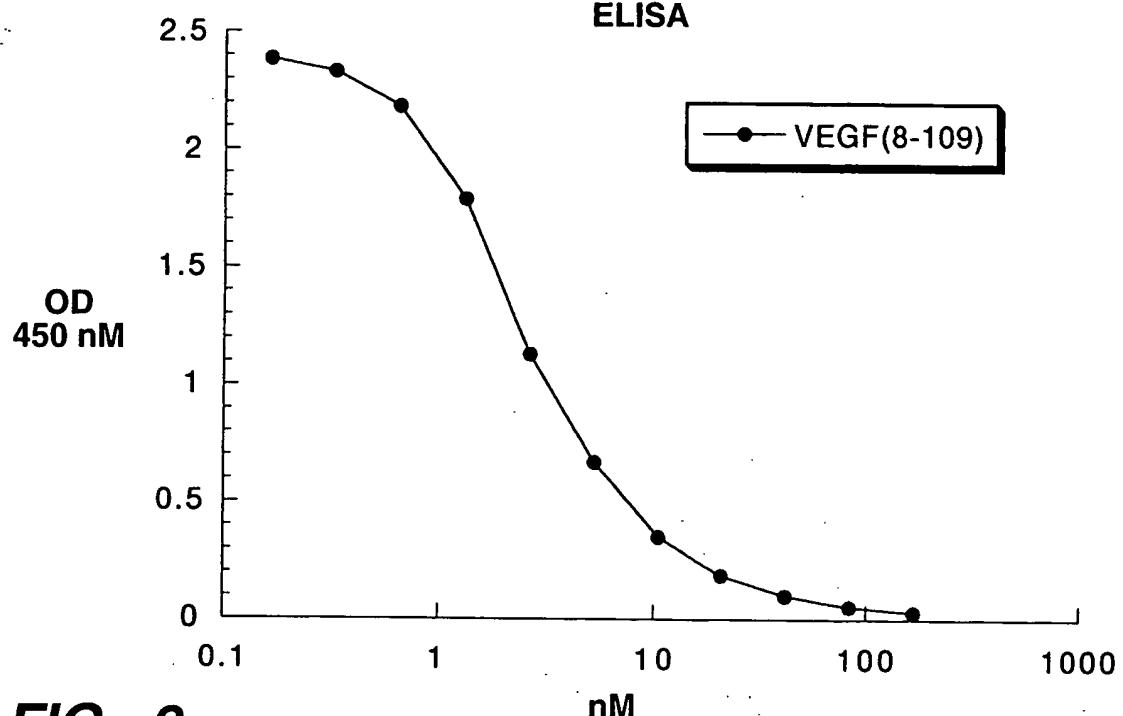


FIG._2

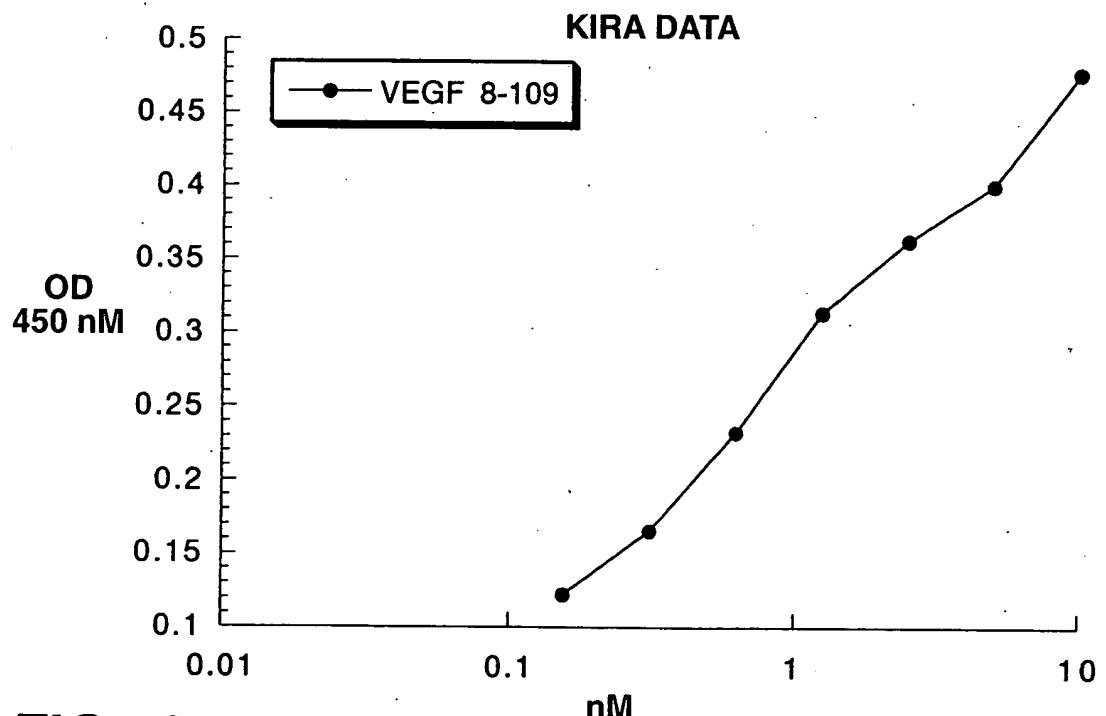


FIG._3



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HUVEC RESPOND TO V8-109

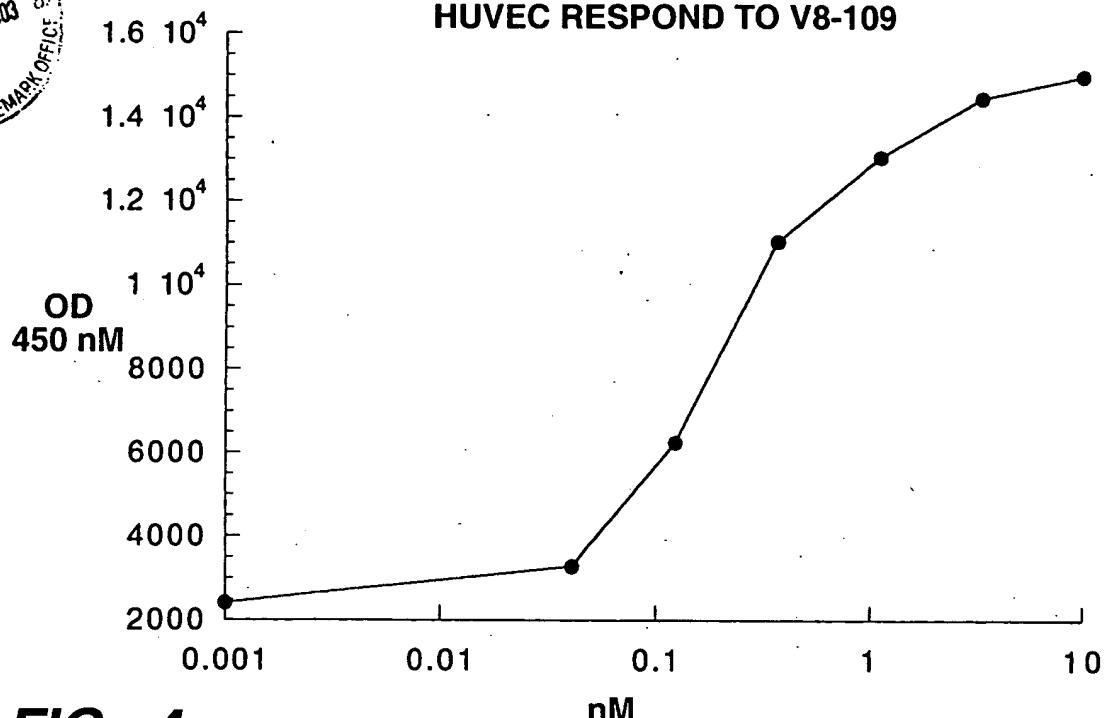


FIG._4

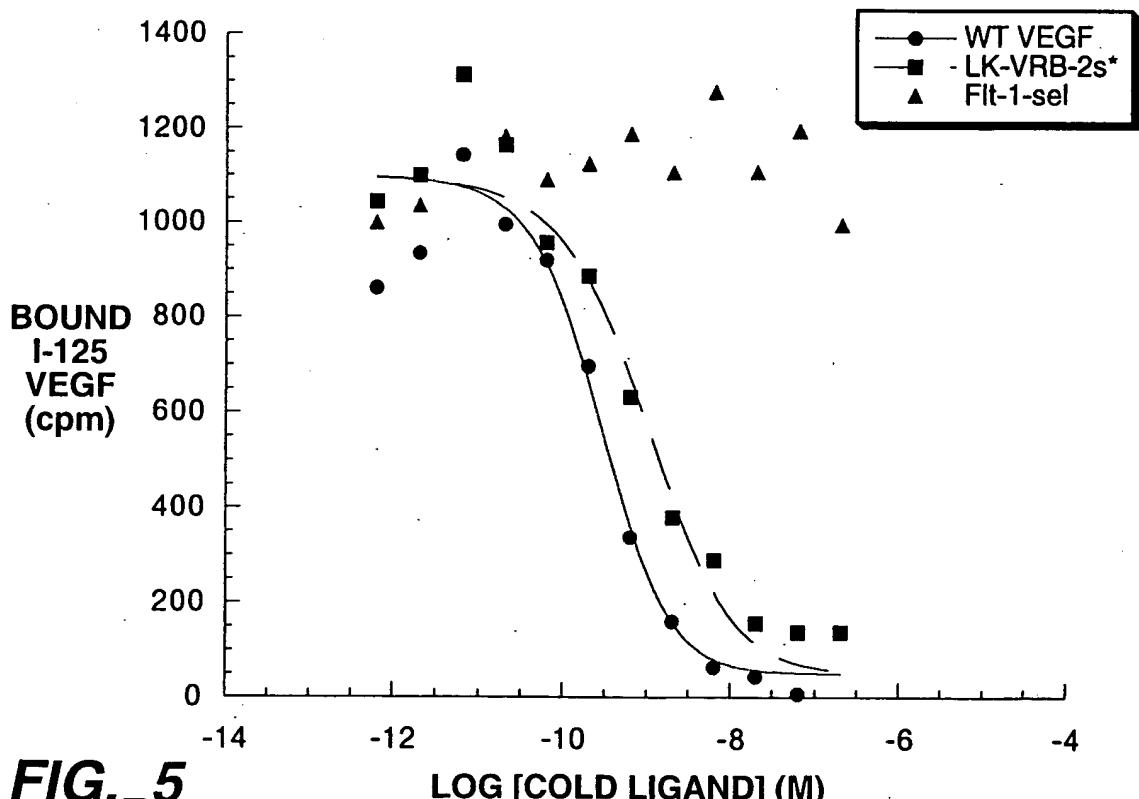


FIG._5



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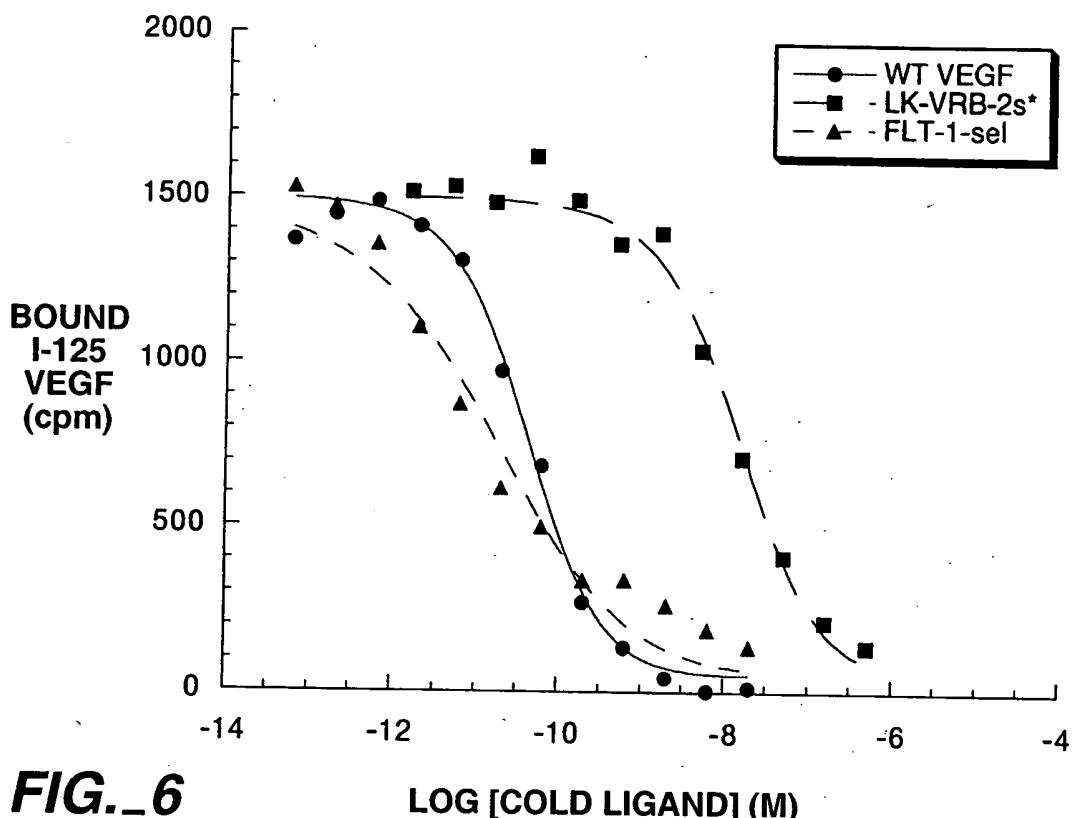


FIG._6



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FOLD REDUCTION IN BINDING OF VEGF ALANINE MUTANTS

RESIDUE	KDR(1-3)	Flt(1-3)
VEGF(1-109)	1 (10nM)	1 (6 nM)
20s Helix:		
Lys 16	1	1
Phe 17*	45	34
Met 18**	5	9
Tyr 21**	19	29
Gln 22**	6	15
Tyr 25**	6	7
40s Loop:		
Ile 43*	21	3
Ile 46*	96	4
Phe 47**	5	3
Lys 48**	1	1
60s Loop:		
Asp 63**	1	8
Glu 64*	10	5
Gly 65**	1	1
Leu 66**	1	10
80s Loop:		
Gln 79*	55	3
Met 81**	9	5
Ile 83*	89	7
His 86**	2	1
Gln 89	1	1
Ile 91	1	1
100s Loop:		
Lys 101	1	1
Glu 103	1	1
Arg 105	1	1
Pro 106	1	1

FIG.-7

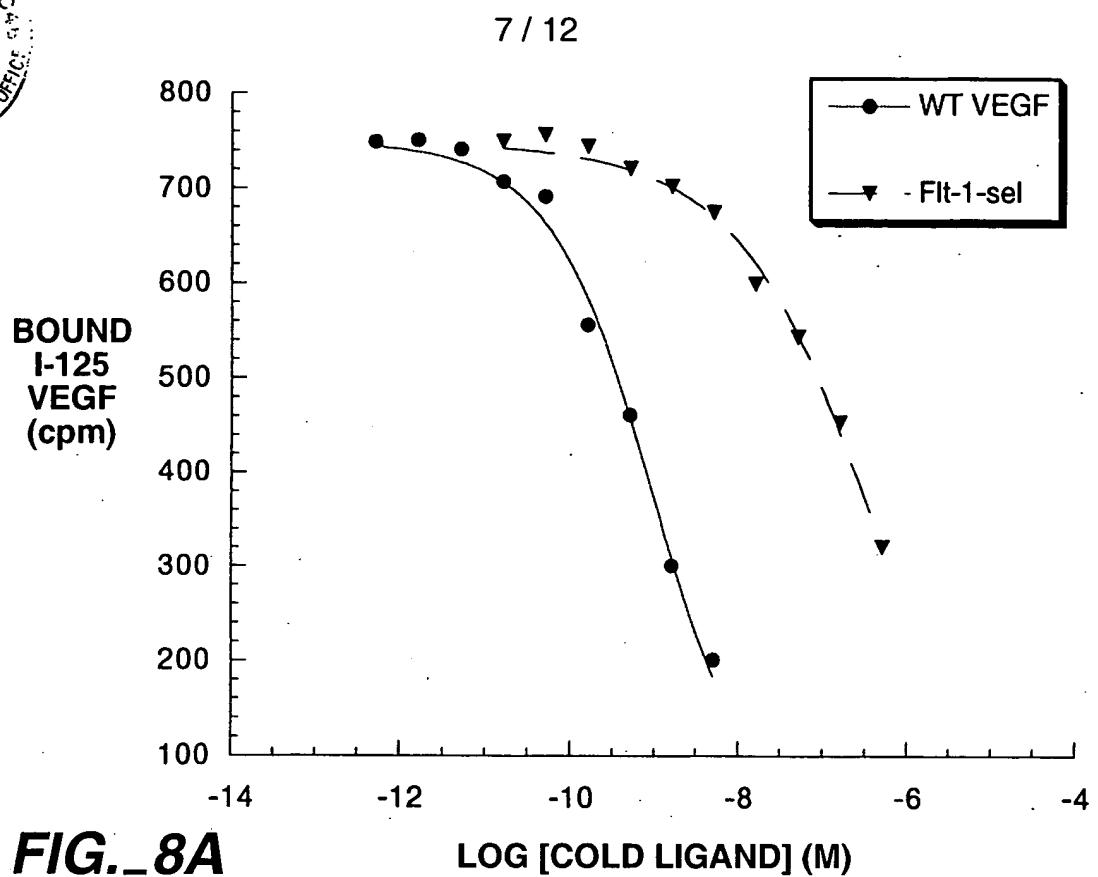


FIG. 8A

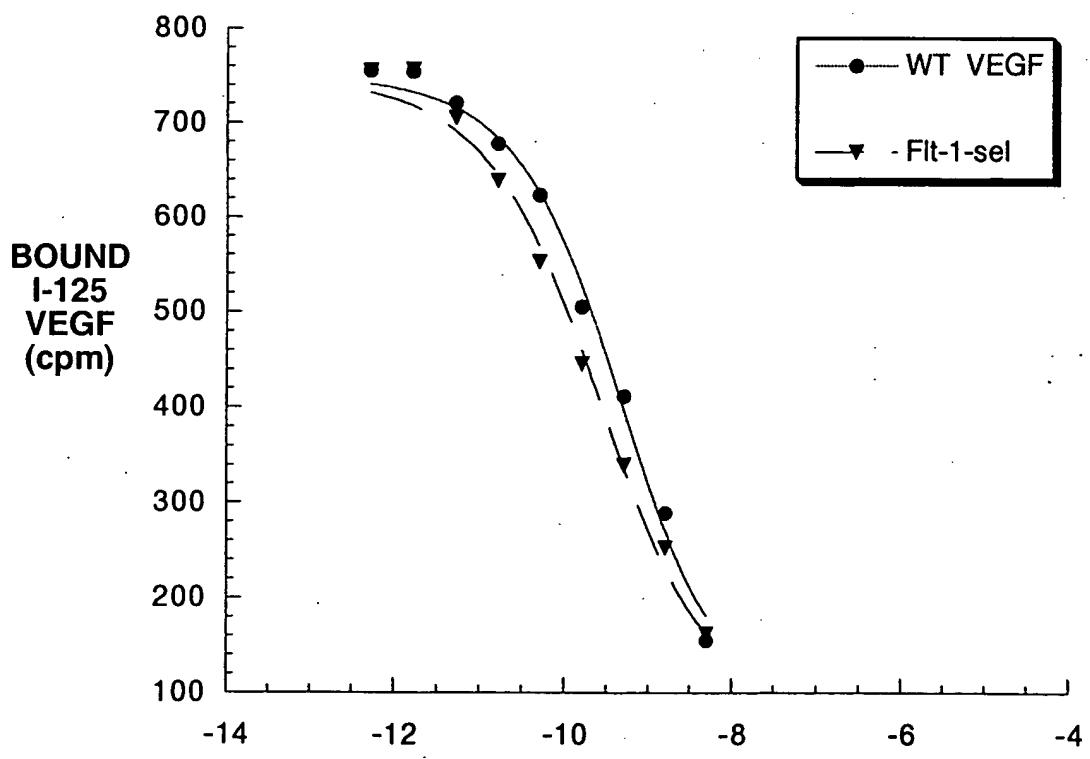


FIG. 8B



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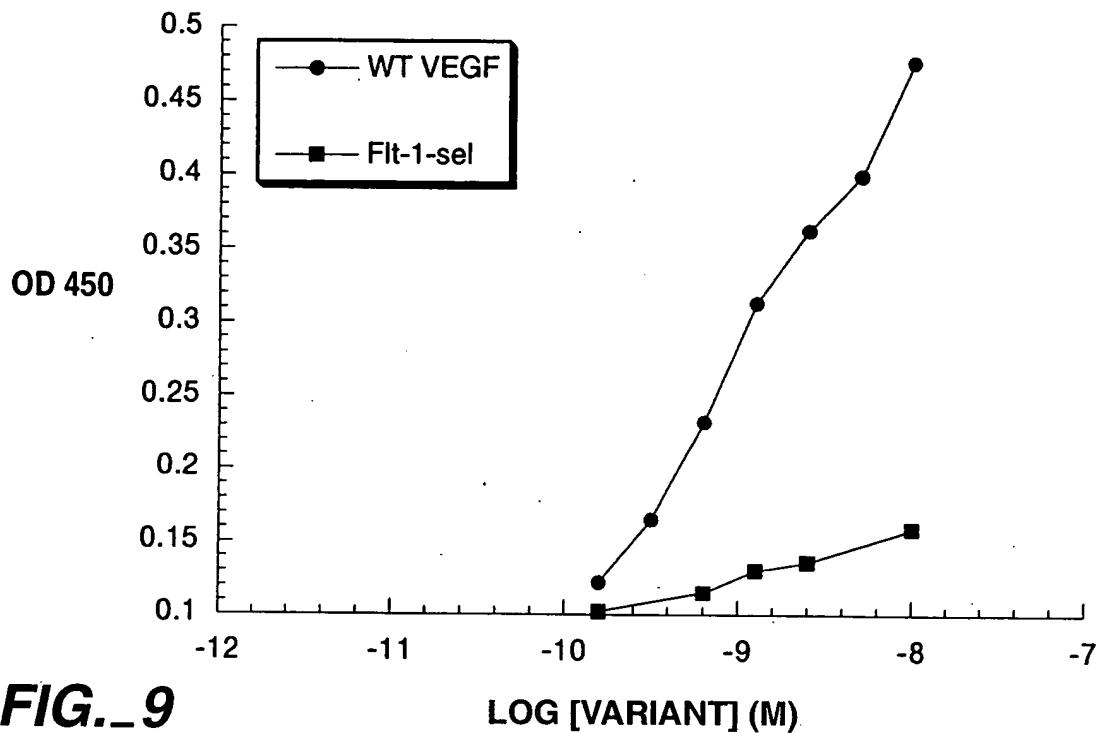


FIG._9

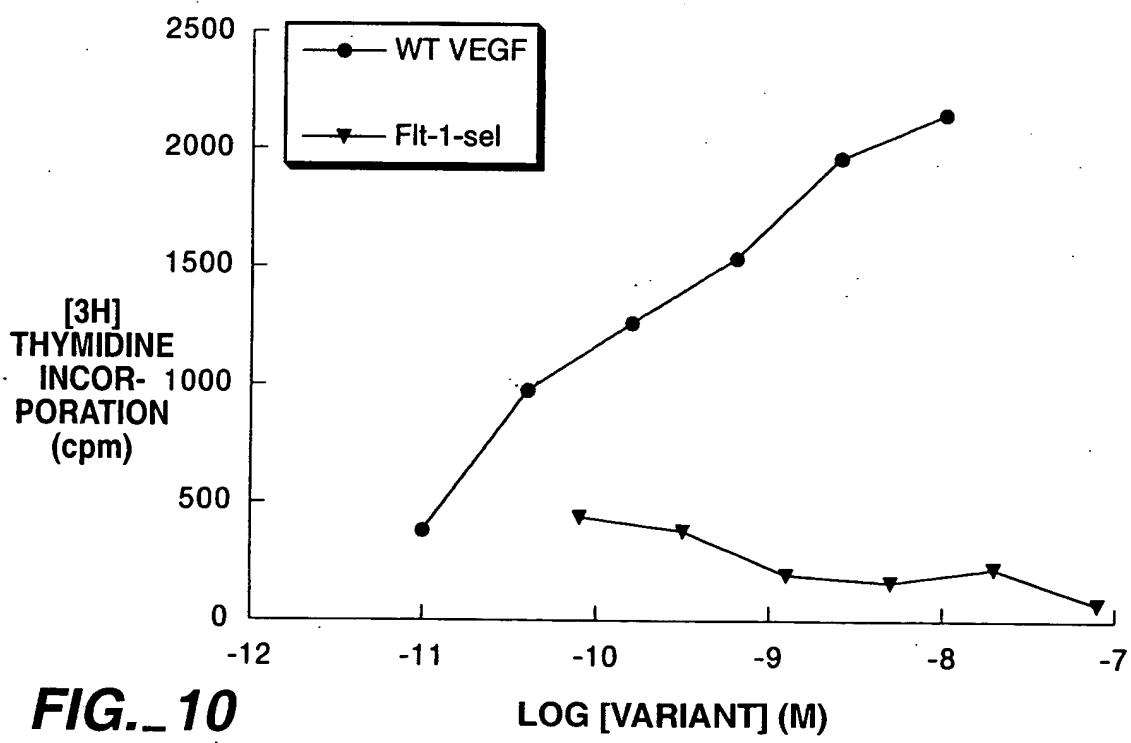


FIG._10

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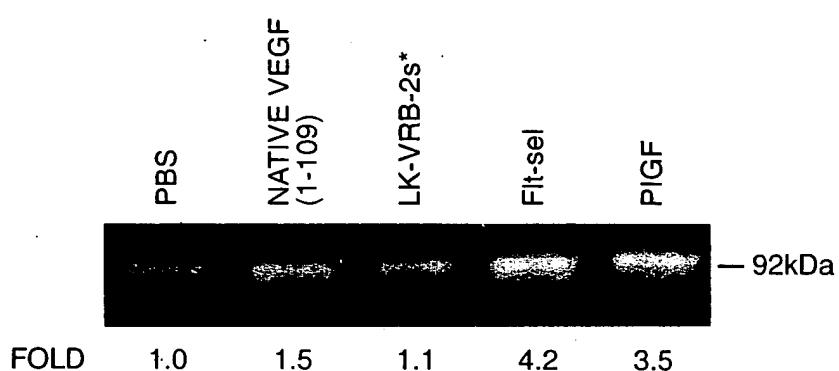


FIG._ 11

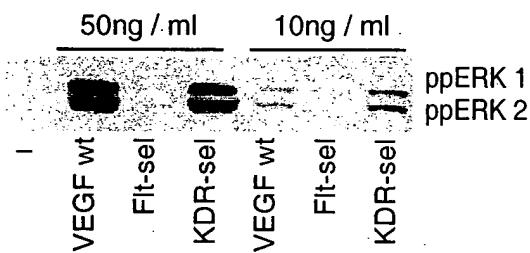


FIG._ 12A

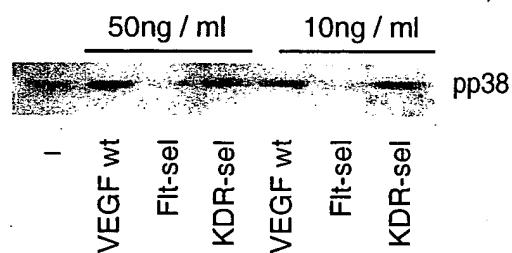


FIG._ 12B

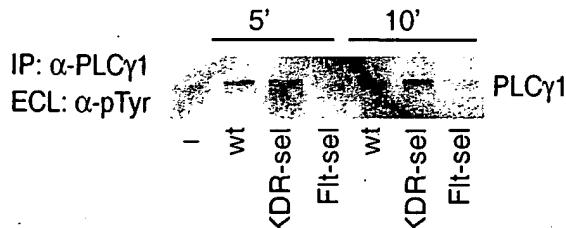


FIG._ 13A

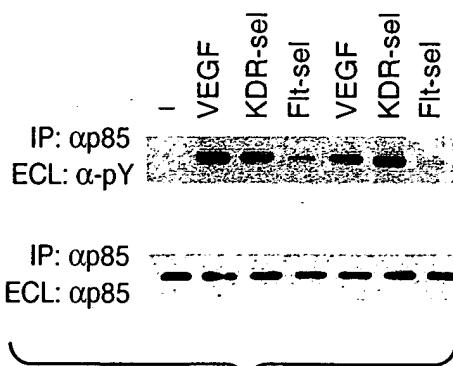


FIG._ 13B



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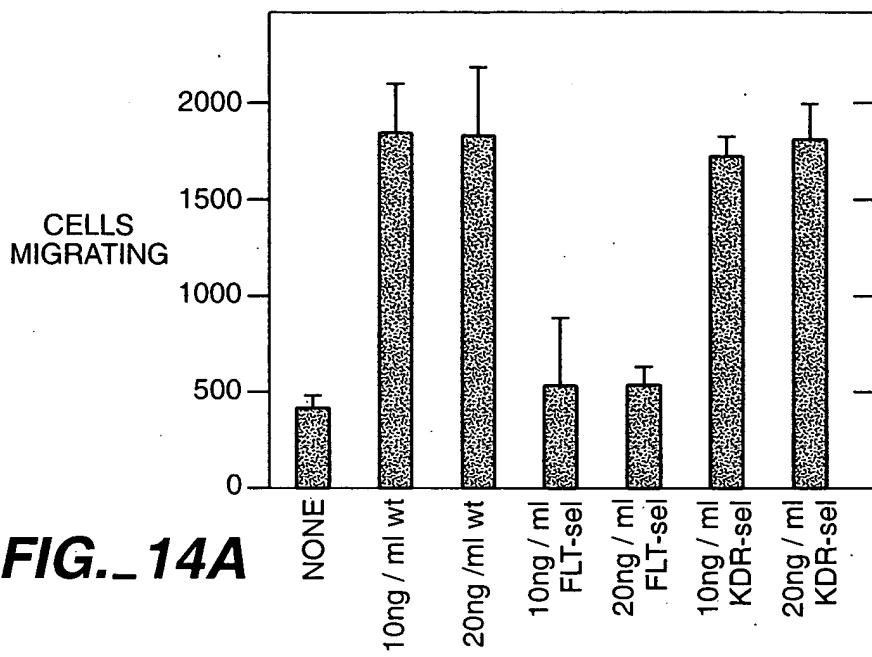


FIG._14A

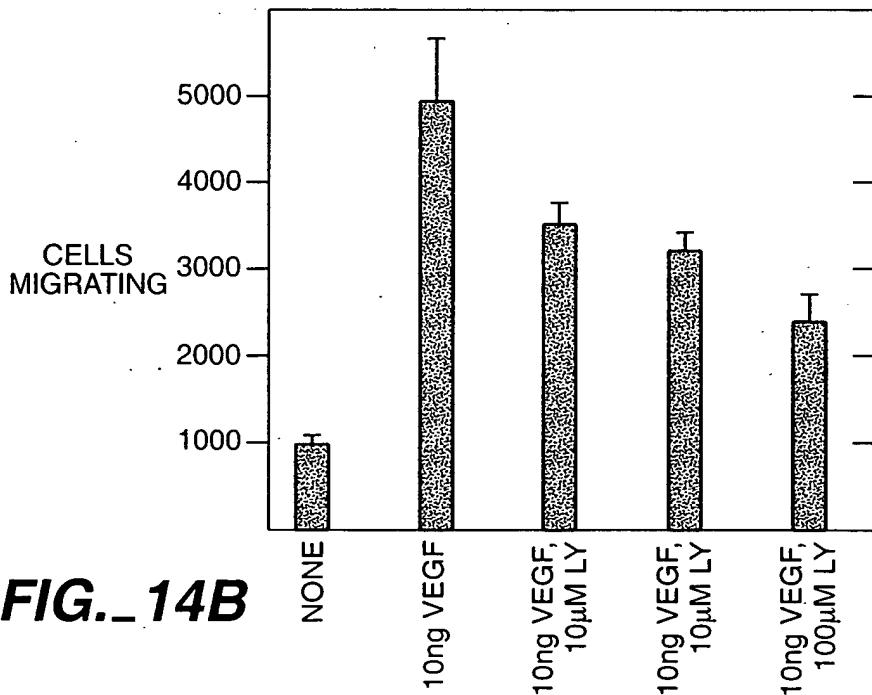


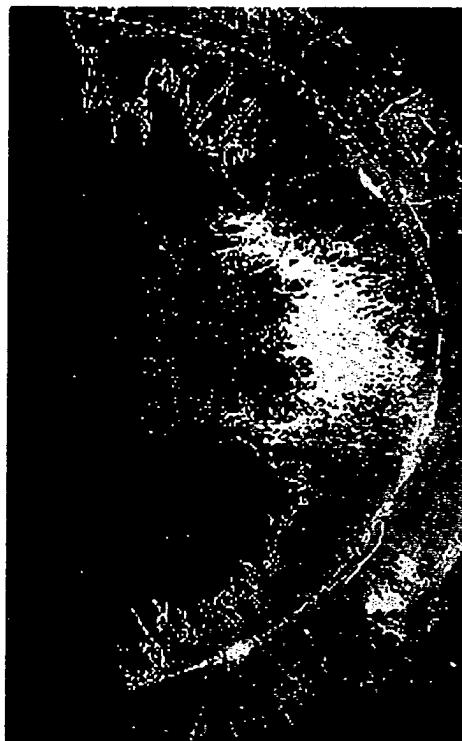
FIG._14B

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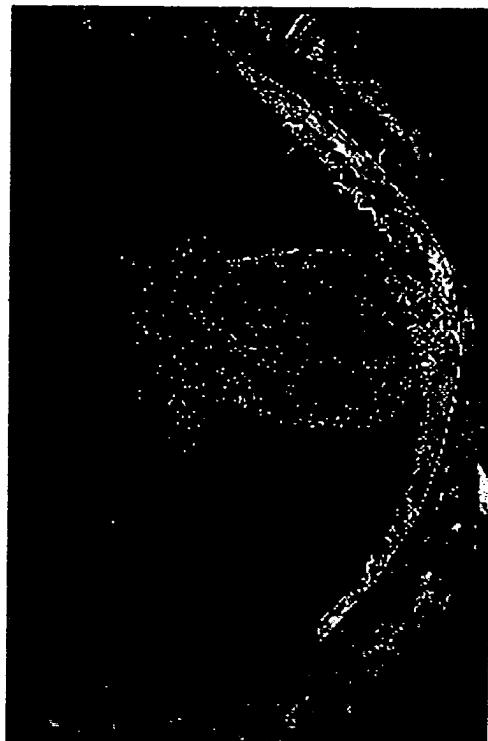
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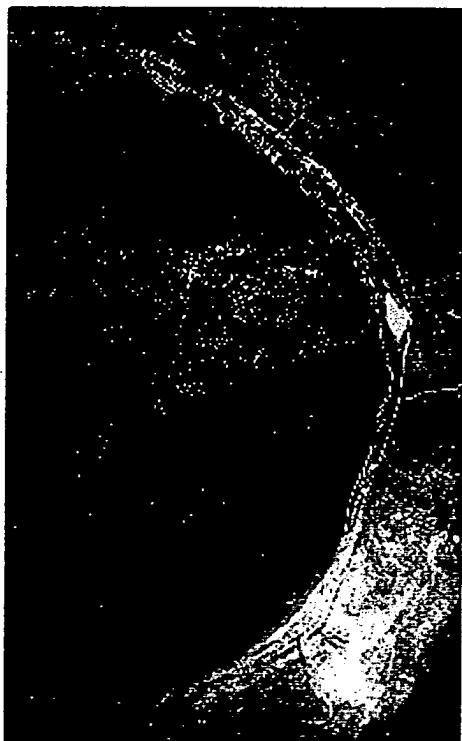
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VEGF



Fit-selective VEGF



Control



KDR-selective VEGF

FIG._15A



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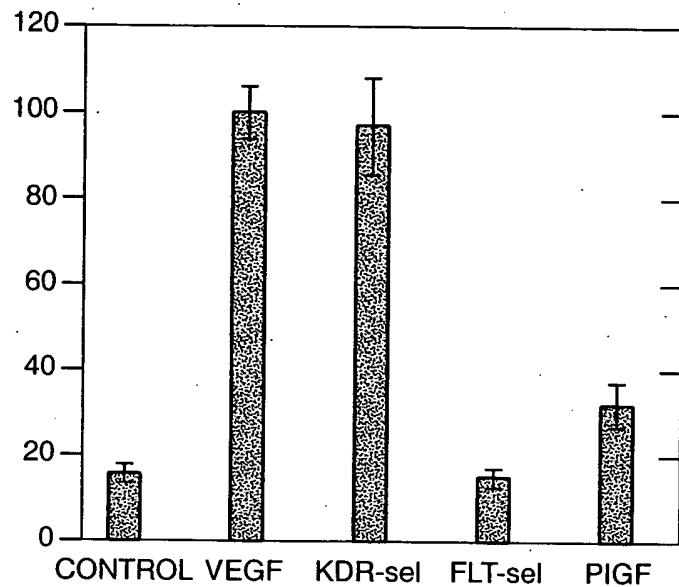


FIG._15B